

# SCORE Search Results Details for Application 10826119 and Search Result 20061115\_093753\_us-10-826-119-3.rge.

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This page gives you Search Results detail for the Application 10826119 and Search Result 20061115\_093753\_us-10-826-119-3.rge.

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2006, 22:42:03 ; Search time 876.6 Seconds  
(without alignments)  
1313.089 Million cell updates/sec

Title: US-10-826-119-3  
Perfect score: 16.8  
Sequence: 1 acrtcaacrtgactkaca 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

- 1: gb\_env:\*
- 2: gb\_pat:\*
- 3: gb\_ph:\*
- 4: gb\_pl:\*
- 5: gb\_pr:\*
- 6: gb\_ro:\*
- 7: gb\_sts:\*
- 8: gb\_sy:\*
- 9: gb\_un:\*
- 10: gb\_vi:\*
- 11: gb\_ov:\*
- 12: gb\_htg:\*
- 13: gb\_in:\*
- 14: gb\_om:\*
- 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	16.8	100.0		331	14	AF039171	AF039171 Ovis arie
2	16.8	100.0		346	14	AF104682	AF104682 Capra ibe
c 3	16.8	100.0		610	7	BV298971	BV298971 S239P6149
4	16.8	100.0		12785	14	AF493541	AF493541 Bos tauru
5	16.8	100.0		12785	14	AF493542	AF493542 Bos tauru
6	16.8	100.0		12785	14	AY308066	AY308066 Bos tauru
7	16.8	100.0		12785	14	AY308067	AY308067 Bos tauru
8	16.8	100.0		12785	14	AY308068	AY308068 Bos tauru
9	16.8	100.0		12785	14	AY308069	AY308069 Bos tauru
10	16.8	100.0		13210	14	AF490528	AF490528 Bos tauru
11	16.8	100.0		13210	14	AF490529	AF490529 Bos tauru
12	16.8	100.0		16322	14	AY684273	AY684273 Bos grunn
13	16.8	100.0		16337	14	AB074962	AB074962 Bos tauru
14	16.8	100.0		16337	14	AB074963	AB074963 Bos tauru
15	16.8	100.0		16337	14	AB074964	AB074964 Bos tauru
16	16.8	100.0		16337	14	AB074965	AB074965 Bos tauru
17	16.8	100.0		16337	14	AB074967	AB074967 Bos tauru
18	16.8	100.0		16337	14	AB074968	AB074968 Bos tauru
19	16.8	100.0		16337	14	AY676865	AY676865 Bos tauru
20	16.8	100.0		16337	14	DQ124387	DQ124387 Bos tauru
21	16.8	100.0		16337	14	DQ124395	DQ124395 Bos tauru
22	16.8	100.0		16338	14	AB074966	AB074966 Bos tauru
23	16.8	100.0		16338	14	AF492351	AF492351 Bos tauru
24	16.8	100.0		16338	14	AY526085	AY526085 Bos tauru
25	16.8	100.0		16338	14	AY676863	AY676863 Bos tauru
26	16.8	100.0		16338	14	MI BTXX	V00654 Bos taurus
27	16.8	100.0		16339	14	AF492350	AF492350 Bos indic
28	16.8	100.0		16339	14	AY676855	AY676855 Bos tauru
29	16.8	100.0		16339	14	AY676856	AY676856 Bos tauru
30	16.8	100.0		16339	14	AY676862	AY676862 Bos tauru
31	16.8	100.0		16339	14	AY676866	AY676866 Bos tauru
32	16.8	100.0		16339	14	AY676867	AY676867 Bos tauru
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36	16.8	100.0		16339	14	AY676873	AY676873 Bos tauru
37	16.8	100.0		16340	14	AY676857	AY676857 Bos tauru
38	16.8	100.0		16340	14	AY676859	AY676859 Bos tauru
39	16.8	100.0		16340	14	AY676860	AY676860 Bos tauru
40	16.8	100.0		16340	14	AY676864	AY676864 Bos tauru
41	16.8	100.0		16340	14	AY676871	AY676871 Bos tauru
42	16.8	100.0		16340	14	DQ124371	DQ124371 Bos tauru
43	16.8	100.0		16340	14	DQ124372	DQ124372 Bos tauru
44	16.8	100.0		16340	14	DQ124373	DQ124373 Bos tauru
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## ALIGNMENTS

RESULT 1

AF039171

LOCUS AF039171 331 bp DNA linear MAM 15-JAN-1999

DEFINITION *Ovis aries* cytochrome oxidase subunit 2 (COII) gene, partial cds; tRNA-Lys gene, complete sequence; ATPase subunit 8 gene, complete cds; and ATPase subunit 6 gene, partial cds, mitochondrial genes for mitochondrial products.

ACCESSION AF039171

VERSION AF039171.1 GI:3769419

KEYWORDS

SOURCE mitochondrion *Ovis aries* (sheep)

ORGANISM *Ovis aries*  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; *Ovis*.

REFERENCE 1 (bases 1 to 331)

AUTHORS Tartaglia, M. and Saulle, E.

TITLE Rapid communication: nucleotide sequence of porcine and ovine tRNA(Lys) and ATPase8 mitochondrial genes

JOURNAL J. Anim. Sci. 76 (8), 2207-2208 (1998)

PUBMED 9734874

REFERENCE 2 (bases 1 to 331)

AUTHORS Tartaglia, M.

TITLE Direct Submission

JOURNAL Submitted (17-DEC-1997) Reparto di Genetica Molecolare, Laboratorio di Biologia Cellulare, Istituto Superiore di Sanita, Viale Regina Elena, 299, Rome 00161, Italy

FEATURES

source Location/Qualifiers

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/organelle="mitochondrion"

/mol\_type="genomic DNA"

/db\_xref="taxon:9940"

/tissue\_type="peripheral blood"

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/gene="COII"

CDS <1..33

/gene="COII"

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/transl\_table=2

/product="cytochrome oxidase subunit 2"

/protein\_id="AAD05066.1"

/db\_xref="GI:3769420"

/translation="YFEKWSASML"

tRNA 37..104

/product="tRNA-Lys"

CDS 106..306

/codon\_start=1

/transl\_table=2

/product="ATPase subunit 8"

/protein\_id="AAD05067.1"

/db\_xref="GI:3769421"

/translation="MPQLDTSTWLTMLSMFLVLFIVFQLKISKHNFYYSPELMTTKM  
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CDS 267..>331

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/transl\_table=2

/product="ATPase subunit 6"

/protein\_id="AAD05068.1"

/db\_xref="GI:3769422"

/translation="MNENLFASFITPMLGLPLVTL"

ORIGIN

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 Best Local Similarity 83.3%; Pred. No. 87;  
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Qy 1 ACRTCAACRTGACTKACA 18  
 ||:|||||:|||||:|  
 Db 121 ACATCAACGTGACTTACA 138

## RESULT 2

AF104682

LOCUS AF104682 346 bp DNA linear MAM 16-MAR-2000

DEFINITION Capra ibex ibex cytochrome oxidase subunit 2 (COII) gene, partial  
 cds; tRNA-Lys gene, complete sequence; ATPase subunit 8 gene,  
 complete cds; and ATPase subunit 6 gene, partial cds, mitochondrial  
 genes for mitochondrial products.

ACCESSION AF104682

VERSION AF104682.1 GI:7248421

## KEYWORDS

SOURCE mitochondrion Capra ibex ibex (Alpine ibex)

ORGANISM Capra ibex ibex

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Caprinae; Capra.

REFERENCE 1 (bases 1 to 346)

AUTHORS Saulle,E., Di Pasquale,S. and Tartaglia,M.

TITLE Rapid communication: nucleotide sequence of chamois, alpine ibex,  
 and red deer tRNA(Lys) and ATPase8 mitochondrial genes

JOURNAL J. Anim. Sci. 77 (12), 3398-3399 (1999)

PUBMED 10641890

REFERENCE 2 (bases 1 to 346)

AUTHORS Saulle,E. and Tartaglia,M.

TITLE Direct Submission

JOURNAL Submitted (06-NOV-1998) Reparto di Genetica Molecolare, Laboratorio  
 di Biologia Cellulare, Istituto Superiore di Sanita, Viale Regina  
 Elena 299, Rome 00161, Italy

## FEATURES

source

Location/Qualifiers

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/organelle="mitochondrion"

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/sub\_species="ibex"

/db\_xref="taxon:80420"

/tissue\_type="peripheral blood"

/country="Italy:Valle d'Aosta, western Alps"

/note="common: Alpine ibex"

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/gene="COII"

CDS

&lt;1. .43

/gene="COII"

/codon\_start=2

/transl\_table=2

/product="cytochrome oxidase subunit 2"

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/db\_xref="GI:7248422"

/translation="PLKHFKEKWSASML"

tRNA

47. .113

/product="tRNA-Lys"

CDS

115. .312

/note="ATPase8"

/codon\_start=1  
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## ORIGIN

Query Match 100.0%; Score 16.8; DB 14; Length 346;  
 Best Local Similarity 83.3%; Pred. No. 88;  
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCAACRTGACTKACA 18  
 ||:|||||:|||||:|||  
 Db 130 ACATCAACATGACTTACA 147

## RESULT 3

BV298971/c

LOCUS BV298971 610 bp DNA linear STS 25-JAN-2005

DEFINITION S239P6149FB2.TO ChinaGrayWolf Canis lupus STS genomic, sequence tagged site.

ACCESSION BV298971

VERSION BV298971.1 GI:57461206

KEYWORDS STS.

SOURCE Canis lupus (gray wolf)

ORGANISM Canis lupus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.

REFERENCE 1 (bases 1 to 610)

AUTHORS Lindblad-Toh, K.

TITLE The genome sequence of Canis familiaris

JOURNAL Unpublished (2004)

## COMMENT

Contact: Kerstin Lindblad-Toh

Whitehead Institute for Biomedical Research, Center for Genome  
 Research

320 Charles Street, Cambridge, MA 02141, USA

Tel: 6172521477

Fax: 6172580903

Email: kersli@genome.wi.mit.edu

Primer A: No sequence submitted

Primer B: No sequence submitted

STS size: 610

Protocol:

WGS-discovery (WGS):

Paired-end low-coverage whole genome shotgun reads were generated  
 from 9 breeds

(German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador  
 Retriever, English

Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese

Water Dog -100,000 each)  
 and five other canids (Chinese, Alaskan, Indian and Spanish Gray Wolf as well as the Californian Coyote).  
 The WGS reads were placed uniquely on the CanFam1.0 boxer assembly and SNP detection was carried out by SSAHA-SNP. 863872 reads were annotated as STSs and 485941 SNPs were annotated with alleles from the boxer and the breed or canid from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.  
 WGA-discovery (WGA) of Boxer/Poodle SNPs:  
 A second set of SNPs was generated using a similar methodology except that the contigs from the 1.5x poodle assembly (Kirkness 2003) were used instead of WGS reads. Since this sequence lacked base quality scores, arbitrary quality scores of phred 40 were assigned before the poodle sequence was placed uniquely on the CanFam1.0 boxer assembly and SNP detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated with alleles from the boxer and the poodle. The validation rate for these SNPs was estimated at approximately TBD%.  
 Internal-WGA-discovery (I-WGA):  
 A third set of SNPs were discovered by comparing reads in the WGA assembly. SNPs were defined as mismatch positions that had a base quality of  $\geq 30$  on both reads in a region that aligned without gaps, and with at most one additional mismatch in the ten flanking bases. For each allele, at least one additional read had to confirm it. 731476 SNPs were annotated with alleles between the two boxer alleles. The validation rate for these SNPs was estimated at approximately TBD%.

FEATURES  
 source Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="ChinaGrayWolf"  
 /db\_xref="taxon:9612"  
 /map="+ 13 22-558 35634917-35634381"  
 /clone\_lib="ChinaGrayWolf"  
 STS  
 <1. .>610  
 ORIGIN

Query Match 100.0%; Score 16.8; DB 7; Length 610;  
 Best Local Similarity 83.3%; Pred. No. 91;  
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACRTCAACRTGACTKACA 18  
 ||:|||||:|||||:|  
 Db 82 ACATCAACATGACTTACA 65

RESULT 4  
 AF493541  
 LOCUS AF493541 12785 bp DNA linear MAM 15-APR-2002  
 DEFINITION Bos taurus isolate D NADH dehydrogenase subunit 1 (ND1), NADH

dehydrogenase subunit 2 (ND2), cytochrome oxidase subunit I (COI), cytochrome oxidase subunit II (COII), ATPase 8, ATPase 6, cytochrome oxidase subunit III (COIII), NADH dehydrogenase subunit 3 (ND3), NADH dehydrogenase subunit 4L (ND4L), NADH dehydrogenase subunit 4 (ND4), NADH dehydrogenase subunit 5 (ND5), NADH dehydrogenase subunit 6 (ND6), and cytochrome b (cytoB) genes, complete cds; mitochondrial genes for mitochondrial products.

ACCESSION AF493541  
 VERSION AF493541.1 GI:20149067  
 KEYWORDS .  
 SOURCE mitochondrion Bos taurus (cattle)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 12785)  
 AUTHORS Wettstein, P.J.  
 TITLE Bos Taurus Mitochondrial Protein Coding Regions  
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 12785)  
 AUTHORS Wettstein, P.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-MAR-2002) Surgery Research, Mayo Foundation, Gugg. Room 5-42B, Rochester, MN 55905, USA

FEATURES Location/Qualifiers  
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 /isolate="D"  
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CDS 1..957  
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          FVHWFPLESGYTLNDTWAKIHFAIMFVGVMNTFFPQHFLGLSGMPRRYSYDPDAYTMW
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Query Match 100.0%; Score 16.8; DB 14; Length 12785;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ACRTCAACRTGACTKACA 18
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Db      5044 ACGTCAACATGACTGACA 5061

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## RESULT 5

AF493542

LOCUS AF493542 12785 bp DNA linear MAM 15-APR-2002

DEFINITION Bos taurus isolate F NADH dehydrogenase subunit 1 (ND1), NADH dehydrogenase subunit 2 (ND2), cytochrome oxidase subunit I (COI), cytochrome oxidase subunit II (COII), ATPase 8, ATPase 6, cytochrome oxidase subunit III (COIII), NADH dehydrogenase subunit 3 (ND3), NADH dehydrogenase subunit 4L (ND4L), NADH dehydrogenase subunit 4 (ND4), NADH dehydrogenase subunit 5 (ND5), NADH dehydrogenase subunit 6 (ND6), and cytochrome b (cytoB) genes, complete cds; mitochondrial genes for mitochondrial products.

ACCESSION AF493542

VERSION AF493542.1 GI:20149081

KEYWORDS

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 12785)

AUTHORS Wettstein,P.J.

TITLE Bos Taurus Mitochondrial Protein Coding Regions

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 12785)

AUTHORS Wettstein,P.J.

TITLE Direct Submission

JOURNAL Submitted (19-MAR-2002) Surgery Research, Mayo Foundation, Gugg.  
 Room 5-42B, Rochester, MN 55905, USA

FEATURES Location/Qualifiers

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gene 1..957

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ERHSRTMILARGLOTLPLMATWLLASLTNLALPPTINLIGELFVVMSTFSWSNIT
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Query Match 100.0%; Score 16.8; DB 14; Length 12785;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ACRTCAACRTGACTKACA 18
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Db      5044 ACGTCAACATGACTGACA 5061

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RESULT 6  
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 LOCUS AY308066 12785 bp DNA circular MAM 30-NOV-2003  
 DEFINITION Bos taurus isolate C31 mitochondrion, partial genome.  
 ACCESSION AY308066  
 VERSION AY308066.1 GI:37960014  
 KEYWORDS

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 12785)

AUTHORS Wettstein, P.J., Lonza, R., Borson, N.D. and McLean, S.

TITLE Direct Submission

JOURNAL Submitted (27-MAY-2003) Dept of Surgery, Mayo Foundation, Gugg. Rm  
537, Rochester, MN 55905, USA

FEATURES

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Query Match 100.0%; Score 16.8; DB 14; Length 12785;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACRTCAACRTGACTKACA 18  
 ||:|||||:||||:|  
 Db 5044 ACGTCAACATGACTGACA 5061

## RESULT 7

AY308067

LOCUS AY308067 12785 bp DNA circular MAM 30-NOV-2003

DEFINITION Bos taurus isolate C33 mitochondrion, partial genome.

ACCESSION AY308067

VERSION AY308067.1 GI:37960028

KEYWORDS

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 12785)

AUTHORS Wettstein, P.J., Lonza, R., Borson, N.D. and McLean, S.

TITLE Direct Submission

JOURNAL Submitted (27-MAY-2003) Dept of Surgery, Mayo Foundation, Gugg. Rm  
 537, Rochester, MN 55905, USA

FEATURES Location/Qualifiers

[start](#) | [next page](#)

SCORE 1.3 BuildDate: 11/17/2006

# SCORE Search Results Details for Application 10826119 and Search Result 20061115\_093753\_us-10-826-119-5.rge.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10826119 and Search Result 20061115\_093753\_us-10-826-119-5.rge.

[start](#) | [next page](#)

[Go Back to previous page](#)

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2006, 22:42:03 ; Search time 1022.7 Seconds  
(without alignments)  
1313.089 Million cell updates/sec

Title: US-10-826-119-5  
Perfect score: 19.8  
Sequence: 1 gacacrtcaacrtgactkaca 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

- 1: gb\_env:\*
- 2: gb\_pat:\*
- 3: gb\_ph:\*
- 4: gb\_pl:\*
- 5: gb\_pr:\*
- 6: gb\_ro:\*
- 7: gb\_sts:\*
- 8: gb\_sy:\*
- 9: gb\_un:\*
- 10: gb\_vi:\*
- 11: gb\_ov:\*
- 12: gb\_htg:\*
- 13: gb\_in:\*
- 14: gb\_om:\*
- 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19.8	100.0	331	14	AF039171	AF039171 Ovis arie
2	19.8	100.0	346	14	AF104682	AF104682 Capra ibe
3	19.8	100.0	12785	14	AF493541	AF493541 Bos tauru
4	19.8	100.0	12785	14	AF493542	AF493542 Bos tauru
5	19.8	100.0	12785	14	AY308066	AY308066 Bos tauru
6	19.8	100.0	12785	14	AY308067	AY308067 Bos tauru
7	19.8	100.0	12785	14	AY308068	AY308068 Bos tauru
8	19.8	100.0	12785	14	AY308069	AY308069 Bos tauru
9	19.8	100.0	13210	14	AF490528	AF490528 Bos tauru
10	19.8	100.0	13210	14	AF490529	AF490529 Bos tauru
11	19.8	100.0	16322	14	AY684273	AY684273 Bos grunn
12	19.8	100.0	16337	14	AB074962	AB074962 Bos tauru
13	19.8	100.0	16337	14	AB074963	AB074963 Bos tauru
14	19.8	100.0	16337	14	AB074964	AB074964 Bos tauru
15	19.8	100.0	16337	14	AB074965	AB074965 Bos tauru
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17	19.8	100.0	16337	14	AB074968	AB074968 Bos tauru
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20	19.8	100.0	16337	14	DQ124395	DQ124395 Bos tauru
21	19.8	100.0	16338	14	AB074966	AB074966 Bos tauru
22	19.8	100.0	16338	14	AF492351	AF492351 Bos tauru
23	19.8	100.0	16338	14	AY526085	AY526085 Bos tauru
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25	19.8	100.0	16338	14	MI BTXX	V00654 Bos taurus
26	19.8	100.0	16339	14	AF492350	AF492350 Bos indic
27	19.8	100.0	16339	14	AY676855	AY676855 Bos tauru
28	19.8	100.0	16339	14	AY676856	AY676856 Bos tauru
29	19.8	100.0	16339	14	AY676862	AY676862 Bos tauru
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44	19.8	100.0	16340	14	DQ124374	DQ124374 Bos tauru
45	19.8	100.0	16340	14	DQ124375	DQ124375 Bos tauru

## ALIGNMENTS

RESULT 1

AF039171  
LOCUS AF039171 331 bp DNA linear MAM 15-JAN-1999  
DEFINITION *Ovis aries* cytochrome oxidase subunit 2 (COII) gene, partial cds; tRNA-Lys gene, complete sequence; ATPase subunit 8 gene, complete cds; and ATPase subunit 6 gene, partial cds, mitochondrial genes for mitochondrial products.  
ACCESSION AF039171  
VERSION AF039171.1 GI:3769419  
KEYWORDS  
SOURCE mitochondrion *Ovis aries* (sheep)  
ORGANISM *Ovis aries*  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; *Ovis*.  
REFERENCE 1 (bases 1 to 331)  
AUTHORS Tartaglia, M. and Saulle, E.  
TITLE Rapid communication: nucleotide sequence of porcine and ovine tRNA(Lys) and ATPase8 mitochondrial genes  
JOURNAL J. Anim. Sci. 76 (8), 2207-2208 (1998)  
PUBMED 9734874  
REFERENCE 2 (bases 1 to 331)  
AUTHORS Tartaglia, M.  
TITLE Direct Submission  
JOURNAL Submitted (17-DEC-1997) Reparto di Genetica Molecolare, Laboratorio di Biologia Cellulare, Istituto Superiore di Sanita, Viale Regina Elena, 299, Rome 00161, Italy  
FEATURES  
source Location/Qualifiers  
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 Best Local Similarity 85.7%; Pred. No. 4.1;  
 Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACACRTCAACRTGACTKACA 21  
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 Db 118 GACACATCAACGTGACTTACA 138

## RESULT 2

AF104682

LOCUS AF104682 346 bp DNA linear MAM 16-MAR-2000

DEFINITION Capra ibex ibex cytochrome oxidase subunit 2 (COII) gene, partial  
 cds; tRNA-Lys gene, complete sequence; ATPase subunit 8 gene,  
 complete cds; and ATPase subunit 6 gene, partial cds, mitochondrial  
 genes for mitochondrial products.

ACCESSION AF104682

VERSION AF104682.1 GI:7248421

KEYWORDS

SOURCE mitochondrion Capra ibex ibex (Alpine ibex)

ORGANISM Capra ibex ibex

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Caprinae; Capra.

REFERENCE 1 (bases 1 to 346)

AUTHORS Saulle,E., Di Pasquale,S. and Tartaglia,M.

TITLE Rapid communication: nucleotide sequence of chamois, alpine ibex,  
 and red deer tRNA(Lys) and ATPase8 mitochondrial genes

JOURNAL J. Anim. Sci. 77 (12), 3398-3399 (1999)

PUBMED 10641890

REFERENCE 2 (bases 1 to 346)

AUTHORS Saulle,E. and Tartaglia,M.

TITLE Direct Submission

JOURNAL Submitted (06-NOV-1998) Reparto di Genetica Molecolare, Laboratorio  
 di Biologia Cellulare, Istituto Superiore di Sanita, Viale Regina  
 Elena 299, Rome 00161, Italy

FEATURES Location/Qualifiers

source

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/tissue\_type="peripheral blood"

/country="Italy:Valle d'Aosta, western Alps"

/note="common: Alpine ibex"

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CDS

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CDS

115. .312

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## ORIGIN

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Best Local Similarity 85.7%;  Pred. No. 4.1;
Matches 18;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

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Db      127 GACACATCAACATGACTTACA 147

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## RESULT 3

AF493541

LOCUS AF493541 12785 bp DNA linear MAM 15-APR-2002

DEFINITION Bos taurus isolate D NADH dehydrogenase subunit 1 (ND1), NADH dehydrogenase subunit 2 (ND2), cytochrome oxidase subunit I (COI), cytochrome oxidase subunit II (COII), ATPase 8, ATPase 6, cytochrome oxidase subunit III (COIII), NADH dehydrogenase subunit 3 (ND3), NADH dehydrogenase subunit 4L (ND4L), NADH dehydrogenase subunit 4 (ND4), NADH dehydrogenase subunit 5 (ND5), NADH dehydrogenase subunit 6 (ND6), and cytochrome b (cytoB) genes, complete cds; mitochondrial genes for mitochondrial products.

ACCESSION AF493541

VERSION AF493541.1 GI:20149067

KEYWORDS

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 12785)

AUTHORS Wettstein,P.J.

TITLE Bos Taurus Mitochondrial Protein Coding Regions

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 12785)

AUTHORS Wettstein,P.J.

TITLE Direct Submission

JOURNAL Submitted (19-MAR-2002) Surgery Research, Mayo Foundation, Gugg. Room 5-42B, Rochester, MN 55905, USA

FEATURES Location/Qualifiers

source

1. .12785

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/mol\_type="genomic DNA"

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/db\_xref="taxon:9913"

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TLSTLITTQEQMWLILPAWPLAMMWFISTLAETNRAPFDLTEGESELVSGFNVEYAAG
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CDS complement(10813..11340)  
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 /db\_xref="GI:20149079"

Query Match 100.0%; Score 19.8; DB 14; Length 12785;  
 Best Local Similarity 85.7%; Pred. No. 7.7;  
 Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACACRTCAACRTGACTKACA 21  
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 Db 5041 GACACGTCAACATGACTGACA 5061

RESULT 4  
 AF493542

LOCUS AF493542 12785 bp DNA linear MAM 15-APR-2002  
 DEFINITION Bos taurus isolate F. NADH dehydrogenase subunit 1 (ND1), NADH  
 dehydrogenase subunit 2 (ND2), cytochrome oxidase subunit I (COI),  
 cytochrome oxidase subunit II (COII), ATPase 8, ATPase 6,

cytochrome oxidase subunit III (COIII), NADH dehydrogenase subunit 3 (ND3), NADH dehydrogenase subunit 4L (ND4L), NADH dehydrogenase subunit 4 (ND4), NADH dehydrogenase subunit 5 (ND5), NADH dehydrogenase subunit 6 (ND6), and cytochrome b (cytoB) genes, complete cds; mitochondrial genes for mitochondrial products.

ACCESSION AF493542  
 VERSION AF493542.1 GI:20149081  
 KEYWORDS .  
 SOURCE mitochondrion Bos taurus (cattle)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 12785)  
 AUTHORS Wettstein, P.J.  
 TITLE Bos Taurus Mitochondrial Protein Coding Regions  
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 12785)  
 AUTHORS Wettstein, P.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-MAR-2002) Surgery Research, Mayo Foundation, Gugg. Room 5-42B, Rochester, MN 55905, USA

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 Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACACRTCAACRTGACTKACA 21  
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## RESULT 5

AY308066

LOCUS AY308066 12785 bp DNA circular MAM 30-NOV-2003

DEFINITION Bos taurus isolate C31 mitochondrion, partial genome.

ACCESSION AY308066

VERSION AY308066.1 GI:37960014

KEYWORDS

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 12785)

AUTHORS Wettstein, P.J., Lonza, R., Borson, N.D. and McLean, S.

TITLE Direct Submission

JOURNAL Submitted (27-MAY-2003) Dept of Surgery, Mayo Foundation, Gugg. Rm  
 537, Rochester, MN 55905, USA

FEATURES Location/Qualifiers

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Query Match 100.0%; Score 19.8; DB 14; Length 12785;  
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 Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db      5041 GACACGTCAACATGACTGACA 5061

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#### RESULT 6 AY308067

LOCUS AY308067 12785 bp DNA circular MAM 30-NOV-2003  
 DEFINITION Bos taurus isolate C33 mitochondrion, partial genome.  
 ACCESSION AY308067  
 VERSION AY308067.1 GI:37960028  
 KEYWORDS .  
 SOURCE mitochondrion Bos taurus (cattle)  
 ORGANISM Bos taurus



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 12785)  
AUTHORS Wettstein, P.J., Lonza, R., Borson, N.D. and McLean, S.  
TITLE Direct Submission  
JOURNAL Submitted (27-MAY-2003) Dept of Surgery, Mayo Foundation, Gugg. Rm  
537, Rochester, MN 55905, USA

FEATURES

	Location/Qualifiers
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gene	1166..2209 /gene="ND2"
CDS	1166..2209 /gene="ND2" /codon_start=1 /transl_table=2 /product="NADH dehydrogenase subunit 2" /protein_id="AAP47842.1" /db_xref="GI:37960030" /translation="MNPIIFIIILLTIMLGTIIVMISSHWLLVWIGFEMNMLAIIPIM MKNHNPRATEASTKYFLTQSTASMLLMMAVIINLMFSGQWTVMKLFNPMASMLMTMAL AMKLGMAPFHFVPEVTQGIPLSSGLILLTWQKLAPMSVLYQIFPSINLNLILTSLVL SILIGGWGGLNQTQLRKIMAYSSIAHMGWMTAVLPYNPTMTLLNLIYIIMTSTMTFM FMANSTTTTSLSHTWNKTPIMTVLILATLLSMGGLPPLSGFMPKWMIIQEMTKNNSI ILPTFMAITALLNLYFYMRLLTYSTTLTMTFSTNNMKMKWQFPLMKMTFLPTMAVLST MMLPLTPMLSVLE"
tRNA	2208..2274 /product="tRNA-Trp"
tRNA	complement(2276..2344) /product="tRNA-Ala"
tRNA	complement(2346..2418) /product="tRNA-Asn"
tRNA	complement(2451..2517) /product="tRNA-Cys"
tRNA	complement(2518..2585)

gene                    /product="tRNA-Tyr"  
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/ gene="COI"  
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/ protein\_id="AAP47843.1"  
/ db\_xref="GI:37960031"  
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GTL LGDDQIYNVVTAHAFVMIFFMVMPIMIGGF GNWL VPLMIGAPDMAFPRMNM SF  
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AINFITTIINMKPPAMSQYQTPLFVWSVMITAVLLLLSLPVL AAGITMLLTDRNLNTT  
FFDPAGGGDPILYQHLFWFFFGHPEVYIILPGFGMISHIVTYYS GKKEPFGYMGMWVA  
MMSIGFLGFIVWAHMMFTVGMDDVTRAYFTSATMIIA IPTGVKVF SWLATLHGGNIKW  
SPAMWALGFIFLFTVGGLTGIVLANSSLDIVLHDTYYVVAHFHYVLSMGAVFAIMGG  
FVHWFP LFSGYTLNDTWAKIHFAIMFVGVMNTFFPQHFLGLSGMPRRYS DYPDAYTMW  
NTISSMGSFISLTAVMLMVFIWEAFASKREVLTVDLTTNLEWLN GCPPPYHTFEEP  
TYVNLK"  
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/ product="tRNA-Ser"  
/ note="codons recognized: UCN"  
trRNA                4205. .4272  
/ product="tRNA-Asp"  
gene                    4274. .4957  
/ gene="COII"  
CDS                    4274. .4957  
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/ codon\_start=1  
/ transl\_table=2  
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/ translation="MAYPMQLGFQDATSPIMEELLHFHDHTLMIVFLISSLVLYIISL  
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FEKWSASML"  
trRNA                4961. .5024

[start](#) | [next page](#)

SCORE 1.3   BuildDate: 11/17/2006

# SCORE Search Results Details for Application 10826119 and Search Result 20061115\_093753\_us-10-826-119-6.rge.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10826119 and Search Result 20061115\_093753\_us-10-826-119-6.rge.

[start](#) | [next page](#)

[Go Back to previous page](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2006, 22:42:03 ; Search time 1071.4 Seconds  
(without alignments)  
1313.089 Million cell updates/sec

Title: US-10-826-119-6  
Perfect score: 20.4  
Sequence: 1 arttctggrttgtgrtaraagt 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
c 1	20.4	100.0	346	14	AF104682	AF104682 Capra ibe
c 2	20.4	100.0	350	14	AF104681	AF104681 Rupicapra
c 3	20.4	100.0	520	14	AB099040	AB099040 Bos tauru
c 4	20.4	100.0	567	14	AB099131	AB099131 Bos tauru
c 5	20.4	100.0	1241	14	CHMTDNA	X65975 C.hircus mi
c 6	20.4	100.0	5351	14	AB075020	AB075020 Bos tauru
c 7	20.4	100.0	12785	14	AF493541	AF493541 Bos tauru
c 8	20.4	100.0	12785	14	AF493542	AF493542 Bos tauru
c 9	20.4	100.0	12785	14	AY308066	AY308066 Bos tauru
c 10	20.4	100.0	12785	14	AY308067	AY308067 Bos tauru
c 11	20.4	100.0	12785	14	AY308068	AY308068 Bos tauru
c 12	20.4	100.0	12785	14	AY308069	AY308069 Bos tauru
c 13	20.4	100.0	13210	14	AF490528	AF490528 Bos tauru
c 14	20.4	100.0	13210	14	AF490529	AF490529 Bos tauru
c 15	20.4	100.0	16337	14	AB074962	AB074962 Bos tauru
c 16	20.4	100.0	16337	14	AB074963	AB074963 Bos tauru
c 17	20.4	100.0	16337	14	AB074964	AB074964 Bos tauru
c 18	20.4	100.0	16337	14	AB074965	AB074965 Bos tauru
c 19	20.4	100.0	16337	14	AB074967	AB074967 Bos tauru
c 20	20.4	100.0	16337	14	AB074968	AB074968 Bos tauru
c 21	20.4	100.0	16337	14	AY676865	AY676865 Bos tauru
c 22	20.4	100.0	16337	14	DQ124387	DQ124387 Bos tauru
c 23	20.4	100.0	16337	14	DQ124395	DQ124395 Bos tauru
c 24	20.4	100.0	16338	14	AB074966	AB074966 Bos tauru
c 25	20.4	100.0	16338	14	AF492351	AF492351 Bos tauru
c 26	20.4	100.0	16338	14	AY526085	AY526085 Bos tauru
c 27	20.4	100.0	16338	14	AY676863	AY676863 Bos tauru
c 28	20.4	100.0	16338	14	MI BTXX	V00654 Bos taurus
c 29	20.4	100.0	16339	14	AF492350	AF492350 Bos indic
c 30	20.4	100.0	16339	14	AY676855	AY676855 Bos tauru
c 31	20.4	100.0	16339	14	AY676856	AY676856 Bos tauru
c 32	20.4	100.0	16339	14	AY676862	AY676862 Bos tauru
c 33	20.4	100.0	16339	14	AY676866	AY676866 Bos tauru
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c 35	20.4	100.0	16339	14	AY676868	AY676868 Bos tauru
c 36	20.4	100.0	16339	14	AY676869	AY676869 Bos tauru
c 37	20.4	100.0	16339	14	AY676870	AY676870 Bos tauru
c 38	20.4	100.0	16339	14	AY676873	AY676873 Bos tauru
c 39	20.4	100.0	16340	14	AY676857	AY676857 Bos tauru
c 40	20.4	100.0	16340	14	AY676859	AY676859 Bos tauru
c 41	20.4	100.0	16340	14	AY676860	AY676860 Bos tauru
c 42	20.4	100.0	16340	14	AY676864	AY676864 Bos tauru
c 43	20.4	100.0	16340	14	AY676871	AY676871 Bos tauru
c 44	20.4	100.0	16340	14	DQ124371	DQ124371 Bos tauru
c 45	20.4	100.0	16340	14	DQ124372	DQ124372 Bos tauru

## ALIGNMENTS

RESULT 1

AF104682/c

LOCUS AF104682 346 bp DNA linear MAM 16-MAR-2000

DEFINITION Capra ibex ibex cytochrome oxidase subunit 2 (COII) gene, partial cds; tRNA-Lys gene, complete sequence; ATPase subunit 8 gene, complete cds; and ATPase subunit 6 gene, partial cds, mitochondrial genes for mitochondrial products.

ACCESSION AF104682

VERSION AF104682.1 GI:7248421

KEYWORDS .

SOURCE mitochondrion Capra ibex ibex (Alpine ibex)

ORGANISM Capra ibex ibex  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Capra.

REFERENCE 1 (bases 1 to 346)

AUTHORS Saulle,E., Di Pasquale,S. and Tartaglia,M.

TITLE Rapid communication: nucleotide sequence of chamois, alpine ibex, and red deer tRNA(Lys) and ATPase8 mitochondrial genes

JOURNAL J. Anim. Sci. 77 (12), 3398-3399 (1999)

PUBMED 10641890

REFERENCE 2 (bases 1 to 346)

AUTHORS Saulle,E. and Tartaglia,M.

TITLE Direct Submission

JOURNAL Submitted (06-NOV-1998) Reparto di Genetica Molecolare, Laboratorio di Biologia Cellulare, Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00161, Italy

FEATURES Location/Qualifiers

source 1..346  
/organism="Capra ibex ibex"  
/organelle="mitochondrion"  
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/sub\_species="ibex"  
/db\_xref="taxon:80420"  
/tissue\_type="peripheral blood"  
/country="Italy:Valle d'Aosta, western Alps"  
/note="common: Alpine ibex"

gene <1..43  
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CDS <1..43  
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/protein\_id="AAF43480.1"  
/db\_xref="GI:7248422"  
/translation="PLKHFEKWSASML"

tRNA 47..113  
/product="tRNA-Lys"

CDS 115..312  
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/codon\_start=1  
/transl\_table=2  
/product="ATPase subunit 8"  
/protein\_id="AAF43481.1"  
/db\_xref="GI:7248423"  
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KQNTPWETKWTKIYLPLLLPL"

CDS 273..>346  
/note="ATPase6"  
/codon\_start=1  
/transl\_table=2

/product="ATPase subunit 6"  
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 /translation="MNENLFTSFITPMVLGLPLITLII"

## ORIGIN

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 Best Local Similarity 81.8%; Pred. No. 28;  
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Qy 1 ARTTCTGGRTTGTGRTARAAGT 22  
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 Db 230 AATTCTGGGTGTGGTAGAAGT 209

## RESULT 2

AF104681/c

LOCUS AF104681 350 bp DNA linear MAM 16-MAR-2000

DEFINITION Rupicapra rupicapra cytochrome oxidase subunit 2 (COII) gene,  
 partial cds; tRNA-Lys gene, complete sequence; ATPase subunit 8  
 gene, complete cds; and ATPase subunit 6 gene, partial cds,  
 mitochondrial genes for mitochondrial products.

ACCESSION AF104681

VERSION AF104681.1 GI:7248417

KEYWORDS

SOURCE mitochondrion Rupicapra rupicapra (chamois)

ORGANISM Rupicapra rupicapra

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Caprinae; Rupicapra.

REFERENCE 1 (bases 1 to 350)

AUTHORS Saulle,E., Di Pasquale,S. and Tartaglia,M.

TITLE Rapid communication: nucleotide sequence of chamois, alpine ibex,  
 and red deer tRNA(Lys) and ATPase8 mitochondrial genes

JOURNAL J. Anim. Sci. 77 (12), 3398-3399 (1999)

PUBMED 10641890

REFERENCE 2 (bases 1 to 350)

AUTHORS Saulle,E. and Tartaglia,M.

TITLE Direct Submission

JOURNAL Submitted (06-NOV-1998) Reparto di Genetica Molecolare, Laboratorio  
 di Biologia Cellulare, Istituto Superiore di Sanita, Viale Regina  
 Elena 299, Rome 00161, Italy

FEATURES Location/Qualifiers.

source

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/organelle="mitochondrion"

/mol\_type="genomic DNA"

/db\_xref="taxon:34869"

/tissue\_type="peripheral blood"

/country="Italy:Valle d'Aosta, western Alps"

/note="common: chamois"

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/gene="COII"

CDS

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/transl\_table=2

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/protein\_id="AAF43477.1"

/db\_xref="GI:7248418"

/translation="PLKYFEKWSASMS"

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## ORIGIN

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Best Local Similarity  81.8%;  Pred. No. 28;
Matches  18;  Conservative  4;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy      1 ARTTCTGGRTTGTGRTARAAGT 22
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Db      231 AATTCTGGGTTGTGGTAGAAGT 210

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## RESULT 3

AB099040/c

LOCUS AB099040 520 bp mRNA linear MAM 12-APR-2003

DEFINITION Bos taurus mitochondrial mRNA for similar to ATP synthase A chain (Protein 6), partial cds, clone: ORCS12732.

ACCESSION AB099040

VERSION AB099040.1 GI:28189830

KEYWORDS

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.

## REFERENCE 1

AUTHORS Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H.;  
Takahashi,T., Imai,K., Hirasawa,A., Shiojima,S., Ikawa,H.,  
Suzuki,Y., Tsujimoto,G., Izaike,Y., Todoroki,J. and Hashizume,K.  
TITLE Characterization of gene expression profiles in early bovine  
pregnancy using a custom cDNA microarray

JOURNAL Mol. Reprod. Dev. 65 (1), 9-18 (2003)

PUBMED 12658628

## REFERENCE 2 (bases 1 to 520)

AUTHORS Tsujimoto,G., Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V.,  
Nakano,H., Konno,T., Ushizawa,K., Takahashi,T., Imai,K.,  
Hirasawa,A., Shiojima,S., Ikawa,H., Suzuki,Y., Izaike,Y.,  
Todoroki,J. and Hashizume,K.

TITLE Direct Submission

JOURNAL Submitted (25-DEC-2002) Gozoh Tsujimoto, National Research  
Institute for Child Health and Development, Department of  
Molecular, Cell Pharmacology; 3-35-31 Taishido, Setagaya, Tokyo  
154-8567, Japan (E-mail:gtsujimoto@nch.go.jp, Tel:81-3-3149-2476,

Fax:81-3-3149-1252)

COMMENT This work was performed to collaborate with Developmental Biology Department, National Institute of Agrobiological Sciences. Address: 2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax: 81-29-838-8633 e-mail: kazuha@affrc.go.jp

This work was funded by Organized Research Combination System (ORCS) project of Ministry of Education, Culture, Sports, Science and Technology.

5' end partial sequence.

FEATURES Location/Qualifiers

source 1. .520

/organism="Bos taurus"

/organelle="mitochondrion"

/mol\_type="mRNA"

/db\_xref="taxon:9913"

/clone="ORCS12732"

/clone\_lib="ORCS bovine utero-placenta cDNA"

/dev\_stage="adult"

/note="mixture of uterus and placenta"

CDS <304. .>468

/codon\_start=2

/transl\_table=2

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/protein\_id="BAC56530.1"

/db\_xref="GI:28189831"

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#### ORIGIN

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Best Local Similarity 81.8%; Pred. No. 26;

Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTTCTGGRTTGTGRTARAAGT 22

|:|||||:||||:|:||||

Db 68 AGTTCTGGATTGTGATAAAAGT 47

#### RESULT 4

AB099131/c

LOCUS AB099131 567 bp RNA linear MAM 21-MAY-2003

DEFINITION Bos taurus mitochondrial RNA, similar to 12S rRNA, clone: ORCS11856.

ACCESSION AB099131

VERSION AB099131.1 GI:28189976

KEYWORDS

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

#### REFERENCE

1

AUTHORS Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H., Takahashi,T., Imai,K., Hirasawa,A., Shiojima,S., Ikawa,H., Suzuki,Y., Tsujimoto,G., Izaike,Y., Todoroki,J. and Hashizume,K.

TITLE Characterization of gene expression profiles in early bovine pregnancy using a custom cDNA microarray

JOURNAL Mol. Reprod. Dev. 65 (1), 9-18 (2003)

PUBMED 12658628

REFERENCE 2 (bases 1 to 567)

AUTHORS Tsujimoto,G., Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V.,



Nakano,H., Konno,T., Ushizawa,K., Takahashi,T., Imai,K.,  
Hirasawa,A., Shiojima,S., Ikawa,H., Suzuki,Y., Izaike,Y.,  
Todoroki,J. and Hashizume,K.

TITLE Direct Submission

JOURNAL Submitted (25-DEC-2002) Gozoh Tsujimoto, National Research  
Institute for Child Health and Development, Department of  
Molecular, Cell Pharmacology; 3-35-31 Taishido, Setagaya, Tokyo  
154-8567, Japan (E-mail:gtsujimoto@nch.go.jp, Tel:81-3-3149-2476,  
Fax:81-3-3149-1252)

COMMENT This work was performed to collaborate with Developmental Biology  
Department, National Institute of Agrobiological Sciences. Address:  
2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:  
81-29-838-8633 e-mail: kazuha@affrc.go.jp  
This work was funded by Organized Research Combination System  
(ORCS) project of Ministry of Education, Culture, Sports, Science  
and Technology.  
5' end partial sequence.

FEATURES Location/Qualifiers  
source 1. .567  
/organism="Bos taurus"  
/organelle="mitochondrion"  
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/note="similar to 12S ribosomal RNA"

#### ORIGIN

Query Match 100.0%; Score 20.4; DB 14; Length 567;  
Best Local Similarity 81.8%; Pred. No. 26;  
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTTCTGGRTTGTGRTARAAGT 22  
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Db 99 AGTTCTGGATTGTGATAAAAGT 78

#### RESULT 5

##### CHMTDNA/c

LOCUS CHMTDNA 1241 bp DNA linear MAM 24-MAY-1996

DEFINITION C.hircus mitochondrial DNA for tRNA(LYS) and F1-ATPase subunits 6  
and 8.

ACCESSION X65975

VERSION X65975.1 GI:11740

KEYWORDS ATPase subunit 6; ATPase subunit 8; mitochondrial DNA; transfer  
RNA-Lys.

SOURCE mitochondrion Capra hircus (goat)

ORGANISM Capra hircus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Caprinae; Capra.

#### REFERENCE

AUTHORS 1 - Dovc,P. and Hecht,W.

TITLE Rapid communication: nucleotide sequence of caprine mitochondrial  
genes for tRNA(Lys) and two subunits of F0-ATPase

JOURNAL J. Anim. Sci. 73 (11), 3493 (1995)

PUBMED 8586610

REFERENCE 2 (bases 1 to 1241)

AUTHORS Dovic, P.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-MAR-1992) P. Dovic, Institut fuer molekulare Tierzucht, Ludwig-Maximilians-Universitaet, Veterinaerstr 13, W-8000 Muenchen 22, FRG

FEATURES Location/Qualifiers  
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     /dev\_stage="adult"  
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## ORIGIN

Query Match 100.0%; Score 20.4; DB 14; Length 1241;  
 Best Local Similarity 81.8%; Pred. No. 23;  
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTTCTGGRTTGTGRTARAAGT 22  
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 Db 292 AATTCTGGGTTGTGGTAGAAGT 271

## RESULT 6

AB075020

LOCUS AB075020 5351 bp mRNA linear MAM 08-JAN-2003  
 DEFINITION Bos taurus Scd mRNA for stearyl-CoA desaturase, complete cds.  
 ACCESSION AB075020  
 VERSION AB075020.1 GI:27544003  
 KEYWORDS  
 SOURCE Bos taurus (cattle)  
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1  
AUTHORS Taniguchi,M., Mannen,H., Shimakura,Y., Oka,A., Watanabe,H.,  
Komatsu,M., Tanaka,K., Harper,G.S. and Tsuji,S.  
TITLE Differences in stearyl-CoA desaturase mRNA levels in muscle  
between Japanese Black and Holstein cattle  
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 5351)  
AUTHORS Taniguchi,M., Mannen,H. and Tsuji,S.  
TITLE Direct Submission  
JOURNAL Submitted (30-NOV-2001) Masaaki Taniguchi, Kobe university,  
Graduate school of science and technology; 1-1, Rokkoudai, Nada,,  
Kobe, Hyogo 657-8501, Japan (E-mail:986d857n@y00.kobe-u.ac.jp,  
Tel:81-78-803-5803, Fax:81-78-803-5801)

FEATURES Location/Qualifiers  
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/country="Japan"  
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ORIGIN

Query Match 100.0%; Score 20.4; DB 14; Length 5351;  
Best Local Similarity 81.8%; Pred. No. 18;  
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTTCTGGRTTGTGRTARAAGT 22  
|:|||||:|||||:|||||  
Db 4 AGTTCTGGATTGTGATAAAAGT 25

## RESULT 7

AF493541/c

LOCUS AF493541 12785 bp. DNA linear MAM 15-APR-2002

DEFINITION Bos taurus isolate D NADH dehydrogenase subunit 1 (ND1), NADH dehydrogenase subunit 2 (ND2), cytochrome oxidase subunit I (COI), cytochrome oxidase subunit II (COII), ATPase 8, ATPase 6, cytochrome oxidase subunit III (COIII), NADH dehydrogenase subunit 3 (ND3), NADH dehydrogenase subunit 4L (ND4L), NADH dehydrogenase subunit 4 (ND4), NADH dehydrogenase subunit 5 (ND5), NADH dehydrogenase subunit 6 (ND6), and cytochrome b (cytoB) genes, complete cds; mitochondrial genes for mitochondrial products.

ACCESSION AF493541

VERSION AF493541.1 GI:20149067

KEYWORDS .

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 12785)

AUTHORS Wettstein,P.J.

TITLE Bos Taurus Mitochondrial Protein Coding Regions

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 12785)

AUTHORS Wettstein,P.J.

TITLE Direct Submission

JOURNAL Submitted (19-MAR-2002) Surgery Research, Mayo Foundation, Gugg. Room 5-42B, Rochester, MN 55905, USA

FEATURES Location/Qualifiers

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Query Match 100.0%; Score 20.4; DB 14; Length 12785;  
 Best Local Similarity 81.8%; Pred. No. 16;  
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Qy 1 ARTTCTGGRTTGTGRTARAAGT 22  
 |:|||||:||||:|:|:|  
 Db 5144 AGTTCTGGATTGTGATAAAAGT 5123

## RESULT 8

AF493542/c

LOCUS AF493542 12785 bp DNA linear MAM 15-APR-2002

DEFINITION Bos taurus isolate F NADH dehydrogenase subunit 1 (ND1), NADH dehydrogenase subunit 2 (ND2), cytochrome oxidase subunit I (COI), cytochrome oxidase subunit II (COII), ATPase 8, ATPase 6, cytochrome oxidase subunit III (COIII), NADH dehydrogenase subunit 3 (ND3), NADH dehydrogenase subunit 4L (ND4L), NADH dehydrogenase subunit 4 (ND4), NADH dehydrogenase subunit 5 (ND5), NADH dehydrogenase subunit 6 (ND6), and cytochrome b (cytoB) genes, complete cds; mitochondrial genes for mitochondrial products.

ACCESSION AF493542

VERSION AF493542.1 GI:20149081

KEYWORDS

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 12785)

AUTHORS Wettstein,P.J.

TITLE Bos Taurus Mitochondrial Protein Coding Regions

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 12785)

AUTHORS Wettstein,P.J.

TITLE Direct Submission

JOURNAL Submitted (19-MAR-2002) Surgery Research, Mayo Foundation, Gugg.  
 Room 5-42B, Rochester, MN 55905, USA

FEATURES Location/Qualifiers

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           /protein_id="AAM12812.1"
           /db_xref="GI:20149092"
           /translation="MMFSSLSLVTLTLLLTMPIMMSFNTYKPSNYPLYVKT AISYAF
ITSMIPTMMFIHSGQELIISNWHWLT IQTLKLSLSFKMDYFSMMFTPVALFVTWSIME
FSMWYMYSDPNINKFFKYLLFLITMLILVTANNLFQLFIGWEGVGIMSFLIGWYWG
RADANTAALQAILYNRIGDIGFILAMAWFLTNLTWDLQQIFMLNPSDSNMPLIGLAL
AATGKSAQFGLHPWLP SAMEGPTPV SALLHSS TMVAGIFLLIRFYPLTENNKYIQSI
TLC LGAITTLEFTAMCALTQNDIKKIIAFSTSSQLGLMMVTIGINQPYLAFLHICTHAF
FKAMLFMCSGSI IHS LNDEQDIRKMGG LFKAMPFTTALIVGSLALTGMPFLTGFYSK
DLIEEAANTS YTNAWALLMTLIATSFTAIYSTRIIFFALLGQPRFPTLVNINENNPLL
INSIKRLLIGSLFAGYIISNNIPPTTIPQMTMPYYLKTALIVTILGFI LALEISNMT
KNLKYHYP SNAFKFSTLLGYFPTIMHRLAPYMNLSMSQKSASSLLDLIWLEAILPKTI
SLAQMKASTLV TNQKGLIKLYFLSFLITILISMILFN FHE"

gene       complement(10813. .11340)
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CDS        complement(10813. .11340)
           /gene="ND6"
           /codon_start=1
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Query Match 100.0%; Score 20.4; DB 14; Length 12785;  
 Best Local Similarity 81.8%; Pred. No. 16;  
 Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTTCTGGRTTGTGRTARAAGT 22  
 |:|||||:||||:|:|  
 Db 5144 AGTTCTGGATTGTGATAAAAGT 5123

RESULT 9  
 AY308066/c  
 LOCUS AY308066 12785 bp DNA circular MAM 30-NOV-2003

DEFINITION Bos taurus isolate C31 mitochondrion, partial genome.  
 ACCESSION AY308066  
 VERSION AY308066.1 GI:37960014  
 KEYWORDS .  
 SOURCE mitochondrion Bos taurus (cattle)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 12785)  
 AUTHORS Wettstein,P.J., Lonza,R., Borson,N.D. and McLean,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-MAY-2003) Dept of Surgery, Mayo Foundation, Gugg. Rm  
 537, Rochester, MN 55905, USA  
 FEATURES Location/Qualifiers  
 source 1..12785  
 /organism="Bos taurus"  
 /organelle="mitochondrion"  
 /mol\_type="genomic DNA"  
 /isolate="C31"  
 /db\_xref="taxon:9913"  
 gene 1..957  
 /gene="ND1"  
 CDS 1..957  
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 /codon\_start=1  
 /transl\_table=2  
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 /protein\_id="AAP47828.1"  
 /db\_xref="GI:37960015"  
 /translation="MFMINILMLIIPILLAVAFLLVERKVLGYMQLRKGPNNVGPYG  
 LLQPIADAIAIKLFIKEPLRPATSSASMFILAPIMALGLALTMWIPLMPYPLINMNLGV  
 LFMLAMSSIAVYSILWSGWASNSKYALIGALRAVAQTISYEVTIAIILLVLLMSGSF  
 TLSTLITTOEQMWLILPAWPLAMWFISTLAETNRAPFDLTEGESELVSGFNVEYAAG  
 PFALFFMAEYANIIMNIFTAILFLGTSHNPHMPELYTINFITKSLLLTMSTFLWIRAS  
 YPRFRYDQLMHLWKNFLPLTLALCMWHVSLPILTSGIPPQT"  
 tRNA 957..1025  
 /product="tRNA-Ile"  
 tRNA complement(1023..1094)  
 /product="tRNA-Gln"

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SCORE 1.3 BuildDate: 11/17/2006

# SCORE Search Results Details for Application 10826119 and Search Result 20061115\_093753\_us-10-826-119-3.rge.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2006, 22:42:03 ; Search time 876.6 Seconds  
(without alignments)  
1313.089 Million cell updates/sec

Title: US-10-826-119-3  
Perfect score: 16.8  
Sequence: 1 acrtcaacrtgactkaca 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

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- 2: gb\_pat:\*
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- 4: gb\_pl:\*
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- 6: gb\_ro:\*
- 7: gb\_sts:\*
- 8: gb\_sy:\*
- 9: gb\_un:\*
- 10: gb\_vi:\*
- 11: gb\_ov:\*
- 12: gb\_htg:\*
- 13: gb\_in:\*
- 14: gb\_om:\*
- 15: gb\_ba:\*

Query Match 100.0%; Score 16.8; DB 14; Length 331;  
 Best Local Similarity 83.3%; Pred. No. 87;  
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACRTCAACRTGACTKACA 18  
 ||:|||||:||||:|  
 Db 121 ACATCAACGTGACTTACA 138

## RESULT 2

AF104682

LOCUS AF104682 346 bp DNA linear MAM 16-MAR-2000

DEFINITION Capra ibex ibex cytochrome oxidase subunit 2 (COII) gene, partial  
 cds; tRNA-Lys gene, complete sequence; ATPase subunit 8 gene,  
 complete cds; and ATPase subunit 6 gene, partial cds, mitochondrial  
 genes for mitochondrial products.

ACCESSION AF104682

VERSION AF104682.1 GI:7248421

## KEYWORDS

SOURCE mitochondrion Capra ibex ibex (Alpine ibex)

ORGANISM Capra ibex ibex

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Caprinae; Capra.

REFERENCE 1 (bases 1 to 346)

AUTHORS Saulle, E., Di Pasquale, S. and Tartaglia, M.

TITLE Rapid communication: nucleotide sequence of chamois, alpine ibex,  
 and red deer tRNA(Lys) and ATPase8 mitochondrial genes

JOURNAL J. Anim. Sci. 77 (12), 3398-3399 (1999)

PUBMED 10641890

REFERENCE 2 (bases 1 to 346)

AUTHORS Saulle, E. and Tartaglia, M.

TITLE Direct Submission

JOURNAL Submitted (06-NOV-1998) Reparto di Genetica Molecolare, Laboratorio  
 di Biologia Cellulare, Istituto Superiore di Sanita, Viale Regina  
 Elena 299, Rome 00161, Italy

## FEATURES

source

Location/Qualifiers

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/organelle="mitochondrion"

/mol\_type="genomic DNA"

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/db\_xref="taxon:80420"

/tissue\_type="peripheral blood"

/country="Italy:Valle d'Aosta, western Alps"

/note="common: Alpine ibex"

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CDS

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/db\_xref="GI:7248422"

/translation="PLKHFEKWSASML"

tRNA

47. .113

/product="tRNA-Lys"

CDS

115. .312

/note="ATPase8"

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273. .>346
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/transl_table=2
/product="ATPase subunit 6"
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/translation="MNENLFTSFITPMVLGLPLITLII"

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## ORIGIN

Query Match 100.0%; Score 16.8; DB 14; Length 346;  
 Best Local Similarity 83.3%; Pred. No. 88;  
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ACRTCAACRTGACTKACA 18
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Db      130 ACATCAACATGACTTACA 147

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## RESULT 3

BV298971/c

LOCUS BV298971 610 bp DNA linear STS 25-JAN-2005

DEFINITION S239P6149FB2.T0 ChinaGrayWolf Canis lupus STS genomic, sequence tagged site.

ACCESSION BV298971

VERSION BV298971.1 GI:57461206

KEYWORDS STS.

SOURCE Canis lupus (gray wolf)

ORGANISM Canis lupus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.

REFERENCE 1 (bases 1 to 610)

AUTHORS Lindblad-Toh, K.

TITLE The genome sequence of Canis familiaris

JOURNAL Unpublished (2004)

## COMMENT

Contact: Kerstin Lindblad-Toh  
 Whitehead Institute for Biomedical Research, Center for Genome  
 Research  
 320 Charles Street, Cambridge, MA 02141, USA  
 Tel: 6172521477  
 Fax: 6172580903  
 Email: kersli@genome.wi.mit.edu  
 Primer A: No sequence submitted  
 Primer B: No sequence submitted  
 STS size: 610  
 Protocol:  
 WGS-discovery (WGS):  
 Paired-end low-coverage whole genome shotgun reads were generated  
 from 9 breeds  
 (German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador  
 Retriever, English  
 Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese

# SCORE Search Results Details for Application 10826119 and Search Result 20061115\_093753\_us-10-826-119-4.rge.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2006, 22:42:03 ; Search time 925.3 Seconds  
(without alignments)  
1313.089 Million cell updates/sec

Title: US-10-826-119-4  
Perfect score: 17.8  
Sequence: 1 tctggrrttgtgrtaraagt 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

- 1: gb\_env:\*
- 2: gb\_pat:\*
- 3: gb\_ph:\*
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- 5: gb\_pr:\*
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- 7: gb\_sts:\*
- 8: gb\_sy:\*
- 9: gb\_un:\*
- 10: gb\_vi:\*
- 11: gb\_ov:\*
- 12: gb\_htg:\*
- 13: gb\_in:\*
- 14: gb\_om:\*
- 15: gb\_ba:\*

AF104682/c

LOCUS AF104682 346 bp DNA linear MAM 16-MAR-2000

DEFINITION Capra ibex ibex cytochrome oxidase subunit 2 (COII) gene, partial cds; tRNA-Lys gene, complete sequence; ATPase subunit 8 gene, complete cds; and ATPase subunit 6 gene, partial cds, mitochondrial genes for mitochondrial products.

ACCESSION AF104682

VERSION AF104682.1 GI:7248421

KEYWORDS

SOURCE mitochondrion Capra ibex ibex (Alpine ibex)

ORGANISM Capra ibex ibex  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Capra.

REFERENCE 1 (bases 1 to 346)

AUTHORS Saulle, E., Di Pasquale, S. and Tartaglia, M.

TITLE Rapid communication: nucleotide sequence of chamois, alpine ibex, and red deer tRNA(Lys) and ATPase8 mitochondrial genes

JOURNAL J. Anim. Sci. 77 (12), 3398-3399 (1999)

PUBMED 10641890

REFERENCE 2 (bases 1 to 346)

AUTHORS Saulle, E. and Tartaglia, M.

TITLE Direct Submission

JOURNAL Submitted (06-NOV-1998) Reparto di Genetica Molecolare, Laboratorio di Biologia Cellulare, Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00161, Italy

FEATURES

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/note="common: Alpine ibex"

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tRNA 47. .113  
/product="tRNA-Lys"

CDS 115. .312  
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/codon\_start=1  
/transl\_table=2  
/product="ATPase subunit 8"  
/protein\_id="AAF43481.1"  
/db\_xref="GI:7248423"  
/translation="MPQLDSTWLTITLSMFLALFIIIFQLKISKHNFYHNPELTTKVLKQNTPWETKWTKIYLP LLLPL"

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/transl\_table=2



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## ORIGIN

Query Match 100.0%; Score 17.8; DB 14; Length 346;  
 Best Local Similarity 84.2%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGGRTTGTGRTARAAGT 19  
 |||||:||||:|:||||  
 Db 227 TCTGGGTTGTGGTAGAAGT 209

## RESULT 2

AF104681/c

LOCUS AF104681 350 bp DNA linear MAM 16-MAR-2000

DEFINITION Rupicapra rupicapra cytochrome oxidase subunit 2 (COII) gene,  
 partial cds; tRNA-Lys gene, complete sequence; ATPase subunit 8  
 gene, complete cds; and ATPase subunit 6 gene, partial cds,  
 mitochondrial genes for mitochondrial products.

ACCESSION AF104681

VERSION AF104681.1 GI:7248417

## KEYWORDS

SOURCE mitochondrion Rupicapra rupicapra (chamois)

ORGANISM Rupicapra rupicapra

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Caprinae; Rupicapra.

REFERENCE 1 (bases 1 to 350)

AUTHORS Saulle,E., Di Pasquale,S. and Tartaglia,M.

TITLE Rapid communication: nucleotide sequence of chamois, alpine ibex,  
 and red deer tRNA(Lys) and ATPase8 mitochondrial genes

JOURNAL J. Anim. Sci. 77 (12), 3398-3399 (1999)

PUBMED 10641890

REFERENCE 2 (bases 1 to 350)

AUTHORS Saulle,E. and Tartaglia,M.

TITLE Direct Submission

JOURNAL Submitted (06-NOV-1998) Reparto di Genetica Molecolare, Laboratorio  
 di Biologia Cellulare, Istituto Superiore di Sanita, Viale Regina  
 Elena 299, Rome 00161, Italy

FEATURES Location/Qualifiers

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 /translation="PLKYFEKWSASMS"

# SCORE Search Results Details for Application 10826119 and Search Result 20061115\_093753\_us-10-826-119-4.rge.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10826119 and Search Result 20061115\_093753\_us-10-826-119-4.rge.

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2006, 22:42:03 ; Search time 925.3 Seconds  
(without alignments)  
1313.089 Million cell updates/sec

Title: US-10-826-119-4  
Perfect score: 17.8  
Sequence: 1 tctggrttgtgrtaraagt 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

- 1: gb\_env:\*
- 2: gb\_pat:\*
- 3: gb\_ph:\*
- 4: gb\_pl:\*
- 5: gb\_pr:\*
- 6: gb\_ro:\*
- 7: gb\_sts:\*
- 8: gb\_sy:\*
- 9: gb\_un:\*
- 10: gb\_vi:\*
- 11: gb\_ov:\*
- 12: gb\_htg:\*
- 13: gb\_in:\*
- 14: gb\_om:\*
- 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	17.8	100.0	346	14	AF104682	AF104682 Capra ibe
c	2	17.8	100.0	350	14	AF104681	AF104681 Rupicapra
c	3	17.8	100.0	520	14	AB099040	AB099040 Bos tauru
c	4	17.8	100.0	567	14	AB099131	AB099131 Bos tauru
c	5	17.8	100.0	1241	14	CHMTDNA	X65975 C.hircus mi
	6	17.8	100.0	5351	14	AB075020	AB075020 Bos tauru
c	7	17.8	100.0	12785	14	AF493541	AF493541 Bos tauru
c	8	17.8	100.0	12785	14	AF493542	AF493542 Bos tauru
c	9	17.8	100.0	12785	14	AY308066	AY308066 Bos tauru
c	10	17.8	100.0	12785	14	AY308067	AY308067 Bos tauru
c	11	17.8	100.0	12785	14	AY308068	AY308068 Bos tauru
c	12	17.8	100.0	12785	14	AY308069	AY308069 Bos tauru
c	13	17.8	100.0	13210	14	AF490528	AF490528 Bos tauru
c	14	17.8	100.0	13210	14	AF490529	AF490529 Bos tauru
c	15	17.8	100.0	16337	14	AB074962	AB074962 Bos tauru
c	16	17.8	100.0	16337	14	AB074963	AB074963 Bos tauru
c	17	17.8	100.0	16337	14	AB074964	AB074964 Bos tauru
c	18	17.8	100.0	16337	14	AB074965	AB074965 Bos tauru
c	19	17.8	100.0	16337	14	AB074967	AB074967 Bos tauru
c	20	17.8	100.0	16337	14	AB074968	AB074968 Bos tauru
c	21	17.8	100.0	16337	14	AY676865	AY676865 Bos tauru
c	22	17.8	100.0	16337	14	DQ124387	DQ124387 Bos tauru
c	23	17.8	100.0	16337	14	DQ124395	DQ124395 Bos tauru
c	24	17.8	100.0	16338	14	AB074966	AB074966 Bos tauru
c	25	17.8	100.0	16338	14	AF492351	AF492351 Bos tauru
c	26	17.8	100.0	16338	14	AY526085	AY526085 Bos tauru
c	27	17.8	100.0	16338	14	AY676863	AY676863 Bos tauru
c	28	17.8	100.0	16338	14	MI BTXX	V00654 Bos taurus
c	29	17.8	100.0	16339	14	AF492350	AF492350 Bos indic
c	30	17.8	100.0	16339	14	AY676855	AY676855 Bos tauru
c	31	17.8	100.0	16339	14	AY676856	AY676856 Bos tauru
c	32	17.8	100.0	16339	14	AY676862	AY676862 Bos tauru
c	33	17.8	100.0	16339	14	AY676866	AY676866 Bos tauru
c	34	17.8	100.0	16339	14	AY676867	AY676867 Bos tauru
c	35	17.8	100.0	16339	14	AY676868	AY676868 Bos tauru
c	36	17.8	100.0	16339	14	AY676869	AY676869 Bos tauru
c	37	17.8	100.0	16339	14	AY676870	AY676870 Bos tauru
c	38	17.8	100.0	16339	14	AY676873	AY676873 Bos tauru
c	39	17.8	100.0	16340	14	AY676857	AY676857 Bos tauru
c	40	17.8	100.0	16340	14	AY676859	AY676859 Bos tauru
c	41	17.8	100.0	16340	14	AY676860	AY676860 Bos tauru
c	42	17.8	100.0	16340	14	AY676864	AY676864 Bos tauru
c	43	17.8	100.0	16340	14	AY676871	AY676871 Bos tauru
c	44	17.8	100.0	16340	14	DQ124371	DQ124371 Bos tauru
c	45	17.8	100.0	16340	14	DQ124372	DQ124372 Bos tauru

## ALIGNMENTS

RESULT 1

AF104682/c  
 LOCUS AF104682 346 bp DNA linear MAM 16-MAR-2000  
 DEFINITION Capra ibex ibex cytochrome oxidase subunit 2 (COII) gene, partial cds; tRNA-Lys gene, complete sequence; ATPase subunit 8 gene, complete cds; and ATPase subunit 6 gene, partial cds, mitochondrial genes for mitochondrial products.  
 ACCESSION AF104682  
 VERSION AF104682.1 GI:7248421  
 KEYWORDS .  
 SOURCE mitochondrion Capra ibex ibex (Alpine ibex)  
 ORGANISM Capra ibex ibex  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Capra.  
 REFERENCE 1 (bases 1 to 346)  
 AUTHORS Saulle,E., Di Pasquale,S. and Tartaglia,M.  
 TITLE Rapid communication: nucleotide sequence of chamois, alpine ibex, and red deer tRNA(Lys) and ATPase8 mitochondrial genes  
 JOURNAL J. Anim. Sci. 77 (12), 3398-3399 (1999)  
 PUBMED 10641890  
 REFERENCE 2 (bases 1 to 346)  
 AUTHORS Saulle,E. and Tartaglia,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-NOV-1998) Reparto di Genetica Molecolare, Laboratorio di Biologia Cellulare, Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00161, Italy  
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 tRNA 47..113  
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 CDS 115..312  
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## ORIGIN

Query Match 100.0%; Score 17.8; DB 14; Length 346;  
 Best Local Similarity 84.2%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGGRTTGTGRTARAAGT 19  
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 Db 227 TCTGGTTGTGGTAGAAGT 209

## RESULT 2

AF104681/c

LOCUS AF104681 350 bp DNA linear MAM 16-MAR-2000

DEFINITION Rupicapra rupicapra cytochrome oxidase subunit 2 (COII) gene,  
 partial cds; tRNA-Lys gene, complete sequence; ATPase subunit 8  
 gene, complete cds; and ATPase subunit 6 gene, partial cds,  
 mitochondrial genes for mitochondrial products.

ACCESSION AF104681

VERSION AF104681.1 GI:7248417

KEYWORDS

SOURCE mitochondrion Rupicapra rupicapra (chamois)

ORGANISM Rupicapra rupicapra

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Caprinae; Rupicapra.

REFERENCE 1 (bases 1 to 350)

AUTHORS Saulle,E., Di Pasquale,S. and Tartaglia,M.

TITLE Rapid communication: nucleotide sequence of chamois, alpine ibex,  
 and red deer tRNA(Lys) and ATPase8 mitochondrial genes

JOURNAL J. Anim. Sci. 77 (12), 3398-3399 (1999)

PUBMED 10641890

REFERENCE 2 (bases 1 to 350)

AUTHORS Saulle,E. and Tartaglia,M.

TITLE Direct Submission

JOURNAL Submitted (06-NOV-1998) Reparto di Genetica Molecolare, Laboratorio  
 di Biologia Cellulare, Istituto Superiore di Sanita, Viale Regina  
 Elena 299, Rome 00161, Italy

FEATURES Location/Qualifiers

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/organelle="mitochondrion"

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/tissue\_type="peripheral blood"

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/note="common: chamois"

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CDS

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CDS       277. .>350
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## ORIGIN

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Query Match      100.0%;  Score 17.8;  DB 14;  Length 350;
Best Local Similarity 84.2%;  Pred. No. 2.3e+02;
Matches 16;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 TCTGGRTTGTGRTARAAGT 19
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Db      228 TCTGGGTTGTGGTAGAAGT 210

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## RESULT 3

AB099040/c

LOCUS AB099040 520 bp mRNA linear MAM 12-APR-2003

DEFINITION Bos taurus mitochondrial mRNA for similar to ATP synthase A chain (Protein 6), partial cds, clone: ORCS12732.

ACCESSION AB099040

VERSION AB099040.1 GI:28189830

KEYWORDS

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.

## REFERENCE

1  
AUTHORS Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H.,  
Takahashi,T., Imai,K., Hirasawa,A., Shiojima,S., Ikawa,H.,  
Suzuki,Y., Tsujimoto,G., Izaike,Y., Todoroki,J. and Hashizume,K.  
TITLE Characterization of gene expression profiles in early bovine  
pregnancy using a custom cDNA microarray

JOURNAL Mol. Reprod. Dev. 65 (1), 9-18 (2003)

PUBMED 12658628

## REFERENCE 2 (bases 1 to 520)

AUTHORS Tsujimoto,G., Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V.,  
Nakano,H., Konno,T., Ushizawa,K., Takahashi,T., Imai,K.,  
Hirasawa,A., Shiojima,S., Ikawa,H., Suzuki,Y., Izaike,Y.,  
Todoroki,J. and Hashizume,K.

TITLE Direct Submission

JOURNAL Submitted (25-DEC-2002) Gozoh Tsujimoto, National Research  
Institute for Child Health and Development, Department of  
Molecular, Cell Pharmacology; 3-35-31 Taishido, Setagaya, Tokyo  
154-8567, Japan (E-mail:gtsujimoto@nch.go.jp, Tel:81-3-3149-2476,

Fax:81-3-3149-1252)

COMMENT This work was performed to collaborate with Developmental Biology Department, National Institute of Agrobiological Sciences. Address: 2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax: 81-29-838-8633 e-mail: kazuha@affrc.go.jp

This work was funded by Organized Research Combination System (ORCS) project of Ministry of Education, Culture, Sports, Science and Technology.

5' end partial sequence.

FEATURES  
 source Location/Qualifiers  
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 CDS  
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 /db\_xref="GI:28189831"  
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#### ORIGIN

Query Match 100.0%; Score 17.8; DB 14; Length 520;  
 Best Local Similarity 84.2%; Pred. No. 2.1e+02;  
 Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGGRTTGTGRTARAAGT 19  
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 Db 65 TCTGGATTGTGATAAAAGT 47

#### RESULT 4

AB099131/c

LOCUS AB099131 567 bp RNA linear MAM 21-MAY-2003

DEFINITION Bos taurus mitochondrial RNA, similar to 12S rRNA, clone: ORCS11856.

ACCESSION AB099131

VERSION AB099131.1 GI:28189976

KEYWORDS

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.

#### REFERENCE

1  
 AUTHORS Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H.,  
 Takahashi,T., Imai,K., Hirasawa,A., Shiojima,S., Ikawa,H.,  
 Suzuki,Y., Tsujimoto,G., Izaike,Y., Todoroki,J. and Hashizume,K.  
 TITLE Characterization of gene expression profiles in early bovine  
 pregnancy using a custom cDNA microarray

JOURNAL Mol. Reprod. Dev. 65 (1), 9-18 (2003)

PUBMED 12658628

REFERENCE 2 (bases 1 to 567)

AUTHORS Tsujimoto,G., Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V.,

Nakano,H., Konno,T., Ushizawa,K., Takahashi,T., Imai,K.,  
Hirasawa,A., Shiojima,S., Ikawa,H., Suzuki,Y., Izaike,Y.,  
Todoroki,J. and Hashizume,K.

TITLE Direct Submission

JOURNAL Submitted (25-DEC-2002) Gozoh Tsujimoto, National Research  
Institute for Child Health and Development, Department of  
Molecular, Cell Pharmacology; 3-35-31 Taishido, Setagaya, Tokyo  
154-8567, Japan (E-mail:gtsujimoto@nch.go.jp, Tel:81-3-3149-2476,  
Fax:81-3-3149-1252)

COMMENT This work was performed to collaborate with Developmental Biology  
Department, National Institute of Agrobiological Sciences. Address:  
2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:  
81-29-838-8633 e-mail: kazuha@affrc.go.jp  
This work was funded by Organized Research Combination System  
(ORCS) project of Ministry of Education, Culture, Sports, Science  
and Technology.  
5' end partial sequence.

FEATURES Location/Qualifiers  
source 1. .567  
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#### ORIGIN

Query Match 100.0%; Score 17.8; DB 14; Length 567;  
Best Local Similarity 84.2%; Pred. No. 2.1e+02;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGGRTTGTGRTARAAGT 19  
|||||:|||||:|:||||  
Db 96 TCTGGATTGTGATAAAAGT 78

#### RESULT 5

CHMTDNA/c

LOCUS CHMTDNA 1241 bp DNA linear MAM 24-MAY-1996  
DEFINITION C.hircus mitochondrial DNA for tRNA(LYS) and F1-ATPase subunits 6  
and 8.

ACCESSION X65975

VERSION X65975.1 GI:11740

KEYWORDS ATPase subunit 6; ATPase subunit 8; mitochondrial DNA; transfer  
RNA-Lys.

SOURCE mitochondrion Capra hircus (goat)

ORGANISM Capra hircus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Caprinae; Capra.

REFERENCE 1

AUTHORS Dovc,P. and Hecht,W.

TITLE Rapid communication: nucleotide sequence of caprine mitochondrial  
genes for tRNA(Lys) and two subunits of F0-ATPase

JOURNAL J. Anim. Sci. 73 (11), 3493 (1995)

PUBMED 8586610

REFERENCE 2 (bases 1 to 1241)



AUTHORS Dovic, P.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-MAR-1992) P. Dovic, Institut fuer molekulare Tierzucht, Ludwig-Maximilians-Universitaet, Veterinaerstr 13, W-8000 Muenchen 22, FRG

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 CDS 177. .374  
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## ORIGIN

Query Match 100.0%; Score 17.8; DB 14; Length 1241;  
 Best Local Similarity 84.2%; Pred. No. 1.8e+02;  
 Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGGRTTGTGRTARAAGT 19  
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 Db 289 TCTGGGTTGTGGTAGAAGT 271

## RESULT 6

AB075020  
 LOCUS AB075020 5351 bp mRNA linear MAM 08-JAN-2003  
 DEFINITION Bos taurus Scd mRNA for stearoyl-CoA desaturase, complete cds.  
 ACCESSION AB075020  
 VERSION AB075020.1 GI:27544003  
 KEYWORDS  
 SOURCE Bos taurus (cattle)  
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.

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REFERENCE 1
AUTHORS Taniguchi,M., Mannen,H., Shimakura,Y., Oka,A., Watanabe,H.,
Komatsu,M., Tanaka,K., Harper,G.S. and Tsuji,S.
TITLE Differences in stearyl-CoA desaturase mRNA levels in muscle
between Japanese Black and Holstein cattle
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 5351)
AUTHORS Taniguchi,M., Mannen,H. and Tsuji,S.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-2001) Masaaki Taniguchi, Kobe university,
Graduate school of science and technology; 1-1, Rokkoudai, Nada,,
Kobe, Hyogo 657-8501, Japan (E-mail:986d857n@y00.kobe-u.ac.jp,
Tel:81-78-803-5803, Fax:81-78-803-5801)

FEATURES
source Location/Qualifiers
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/haplotype="G"
/country="Japan"
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5'UTR 1. .387
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CDS 388. .1467
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HKFSETDADPHNSRRGFFFSHVGLLVKHPAVKEKGSTLNLSDLRAEKLVMFQRRYY
KPGVLLLCFILPTLVPWYLWDETFFQNSLFFATLFRYALGLNVTWLVNSAAHMYGYRPY
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DRKKVSKAAAILARIIRTGEESYKSG"
3'UTR 1468. .5351
/gene="Scd"
polyA_signal 5098. .5103
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ORIGIN

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Query Match      100.0%;  Score 17.8;  DB 14;  Length 5351;
Best Local Similarity 84.2%;  Pred. No. 1.5e+02;
Matches 16;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy 1 TCTGGRTTGTGRTARAAGT 19
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Db 7 TCTGGATTGTGATAAAAGT 25

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## RESULT 7

AF493541/c

LOCUS AF493541 12785 bp DNA linear MAM 15-APR-2002

DEFINITION Bos taurus isolate D NADH dehydrogenase subunit 1 (ND1), NADH dehydrogenase subunit 2 (ND2), cytochrome oxidase subunit I (COI), cytochrome oxidase subunit II (COII), ATPase 8, ATPase 6, cytochrome oxidase subunit III (COIII), NADH dehydrogenase subunit 3 (ND3), NADH dehydrogenase subunit 4L (ND4L), NADH dehydrogenase subunit 4 (ND4), NADH dehydrogenase subunit 5 (ND5), NADH dehydrogenase subunit 6 (ND6), and cytochrome b (cytoB) genes, complete cds; mitochondrial genes for mitochondrial products.

ACCESSION AF493541

VERSION AF493541.1 GI:20149067

KEYWORDS .

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 12785)

AUTHORS Wettstein, P.J.

TITLE Bos Taurus Mitochondrial Protein Coding Regions

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 12785)

AUTHORS Wettstein, P.J.

TITLE Direct Submission

JOURNAL Submitted (19-MAR-2002) Surgery Research, Mayo Foundation, Gugg. Room 5-42B, Rochester, MN 55905, USA

FEATURES Location/Qualifiers

source

1. .12785

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CDS

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/protein\_id="AAM12789.1"

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TLSTLITTOEQMWLILPAWPLAMWFISTLAETNRAPFDLTEGESELVSGFNVEYAAG

PFALFFMAEYANIIMNIFTAILFLGTSHNPHMPELYTINFTIKSLLLTMSTFLWIRAS

YPRFRYDQIMHLLWKNFLPLTLALCMWHVSLPILTSGIPPQT"

gene

1166. .2209

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CDS

1166. .2209

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AMKLGMAPFHFVPEVTQGIPLSSGLILLTWQKLAPMSVLYQIFPSINLNLILTSLVLSILIGGWGGLNQTQLRKIMAYSSIAHMGWMTAVLPYNPTMTLLNLIYIIMTSTMFTMFMANSTTTTSLSHTWNKTPIMTVLILATLLSMGGLPPLSGFMPKWMIIQEMTKNNSIILPTFMAITALLNLYFYMRLTYSTTLTMFPSTNNMKMKWQFPLMKMTFLPTMVVLSTMMLPLTPMLSVLE"

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CDS 5190. .5870  
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/db\_xref="GI:20149073"  
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gene 5870. .6673  
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CDS 5870. .6673  
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Db      5141 TCTGGATTGTGATAAAAGT 5123

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## RESULT 8

AF493542/c

LOCUS AF493542 12785 bp DNA linear MAM 15-APR-2002

DEFINITION Bos taurus isolate F.NADH dehydrogenase subunit 1 (ND1), NADH dehydrogenase subunit 2 (ND2), cytochrome oxidase subunit I (COI), cytochrome oxidase subunit II (COII), ATPase 8, ATPase 6, cytochrome oxidase subunit III (COIII), NADH dehydrogenase subunit 3 (ND3), NADH dehydrogenase subunit 4L (ND4L), NADH dehydrogenase subunit 4 (ND4), NADH dehydrogenase subunit 5 (ND5), NADH dehydrogenase subunit 6 (ND6), and cytochrome b (cytoB) genes, complete cds; mitochondrial genes for mitochondrial products.

ACCESSION AF493542

VERSION AF493542.1 GI:20149081

KEYWORDS

SOURCE mitochondrion Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 12785)

AUTHORS Wettstein,P.J.

TITLE Bos Taurus Mitochondrial Protein Coding Regions

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 12785)

AUTHORS Wettstein,P.J.

TITLE Direct Submission

JOURNAL Submitted (19-MAR-2002) Surgery Research, Mayo Foundation, Gugg. Room 5-42B, Rochester, MN 55905, USA

FEATURES Location/Qualifiers

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Best Local Similarity 84.2%; Pred. No. 1.3e+02;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 5141 TCTGGATTGTGATAAAAGT 5123

RESULT 9  
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DEFINITION Bos taurus isolate C31 mitochondrion, partial genome.  
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 VERSION AY308066.1 GI:37960014  
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 SOURCE mitochondrion Bos taurus (cattle)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 12785)  
 AUTHORS Wettstein, P.J., Lonza, R., Borson, N.D. and McLean, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-MAY-2003) Dept of Surgery, Mayo Foundation, Gugg. Rm  
 537, Rochester, MN 55905, USA  
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[start](#) | [next page](#)

SCORE 1.3 BuildData: 11/17/2006